

SEQUENCE LISTING



<110> Marks, James D
Poul, Marie A

<120> INTERNALIZING ERBB2 ANTIBODIES

<130> 2500.114US1

<140> 09/250,056

<141> 1999-02-12

<150> 60/082,953

<151> 1998-03-04

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 246

<212> PRT

<213> Artificial Sequence

a

<220>

<223> Description of Artificial Sequence: scFv F5 amino
acid sequence

AA

<220>

<221> DOMAIN

<222> (31)..(35)

<223> VH-CDR1

<220>

<221> DOMAIN

<222> (50)..(66)

<223> VH-CDR2

<220>

<221> DOMAIN

<222> (99)..(108)

<223> VH-CDR-3

<220>

<221> DOMAIN

<222> (157)..(170)

<223> VL-CDR1

<220>

<221> DOMAIN

<222> (186)..(192)

<223> VL-CDR2

<220>

<221> DOMAIN

<222> (225)..(235)

<223> VL-CDR3

<400> 1

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Arg Gly Asp Asn Thr Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Met Thr Ser Asn Ala Phe Ala Phe Asp Tyr Trp Gly Gln Gly

100

105

110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

115

120

125

Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val

130

135

140

Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser

145

150

155

160

Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln Gln Leu Pro

165

170

175

Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser

180

185

190

Gly Val Pro Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser

195	200	205
Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys		
210	215	220
Gln Phe Tyr Asp Ser Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr		
225	230	235 240
Lys Leu Thr Val Leu Gly		
245		

<210> 2
 <211> 242
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: scC1 Fv amino
 acid sequence

<220>
 <221> DOMAIN
 <222> (31)..(35)
 <223> VH-CDR2

<220>
 <221> DOMAIN
 <222> (50)..(66)
 <223> VH-CDR2

<220>
 <221> DOMAIN
 <222> (99)..(108)
 <223> VH-CDR3

<220>
 <221> DOMAIN
 <222> (157)..(167)
 <223> VL-CDR1

<220>
 <221> DOMAIN
 <222> (184)..(190)
 <223> VL-CDR2

<220>
 <221> DOMAIN

<222> (223)..(231)

<223> VL-CDR3

<400> 2

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Gly Trp Xaa Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Ser Ser Arg Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Met Asp Ala Ser Gly Ser Tyr Phe Asn Phe Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Glu Thr Thr Leu Thr Gln Ser Pro Ser Phe
130 135 140

Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Pro Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asn Ser Tyr Pro Leu Ser Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Arg

<210> 3

<211> 738

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: scF5 single
chain Ab

<220>

<221> misc_feature

<222> (91)..(105)

<223> VH-CFR1

<220>

<221> misc_feature

<222> (148)..(198)

<223> VH-CDR2

<220>

<221> misc_difference

<222> (295)..(324)

<223> VH-CDR3

<220>

<221> misc_feature

<222> (469)..(510)

<223> VL-CDR1

<220>

<221> misc_feature

<222> (556)..(576)

<223> VL-CDR2

<220>

<221> misc_feature

<222> (673)..(703)

<223> VL-CDR3

<400> 3

caggtgcagc tgggtggagtc tggggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttcgc agctatgccca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggtc gtggtgataa cacatactac 180

```

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgttt attactgtgc gaaaatgaca 300
agtaacgcgt tcgcatttga ctactggggc caggggaaccc tggtcaccgt ctctcaggt 360
ggagggcggtt caggcggagg tggctctggc ggtggcggat cgcagtctgt gttgacgcag 420
ccgccctcag tgtctggggc cccagggcag agggtcacca tctcctgcac tgggagcagc 480
tccaacatcg gggcaggtta tgggtgtacac tggtagcagc agcttccagg aacagccccc 540
aaactcctca tctatggtaa caccaatcgg ccctcagggg tccctgaccg attctctggc 600
ttcaagtctg gcacctcagc ctccctggcc atcactgggc tccaggctga ggatgaggct 660
gattattact gccagttcta tgacagcagc ctgagtgggt ggggtgttcg cggaggggacc 720
aagctgaccg tgctaggt                                     738

```

<210> 4

<211> 726

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: scC1 single
chain Ab

<220>

<221> misc_feature

<222> (91)..(105)

<223> VH-CDR1

<220>

<221> misc_feature

<222> (148)..(198)

<223> VH-CDR2

<220>

<221> misc_feature

<222> (295)..(324)

<223> VH-CDR3

<220>

<221> misc_feature

<222> (472)..(504)

<223> VL-CDR1

<220>

<221> misc_feature

<222> (550)..(570)

<223> VL-CDR2

<220>

<221> misc_feature

<222> (667)..(693)

<223> VL-CDR3

<400> 4

```
caggtgcagc tgggtggagtc tgggggagggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagc agctatgcc a tgggctgggt ncgccaggct 120
ccagggaagg ggctggagtg ggtctcatca attagtggca gtagtagata catatattac 180
gcagactccg tgaagggccg gttcaccatc tcccgagaca attccaagaa cacgctgtat 240
ctgcaaata ga acagcctgcg agccgaggac acggccgttt attactgtgc gaaaatggat 300
gcttcgggga gttatttta tttctggggc cagggcaccc tggtcaccgt ctctcagggt 360
ggaggcgggt caggcggagg tggctctggc ggtggcggat cggaaacgac actcacgcag 420
tctccatcct tcctgtctgc atttgtagga gacagaatca ccatcacttg ccggggccagt 480
ccgggcatta ggaattattt agcctgggat cagcaaaaac cagggaagc ccctaagctc 540
ctgatctatg ctgcacccac tttgcaaagt ggggtcccat caaggttcag cggcagtgga 600
tctgggacag attttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat 660
tattgtcaac aatataatag ttaccctctc agtttcggcg gagggaccaa ggtggagatc 720
aaacgt 726
```